RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: ___10/783, 415A___

Source: ___IFW16___

Date Processed by STIC: ___09/14/2005___

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RAW SEQUENCE LISTING   DATE: 09/14/2005
PATENT APPLICATION: US/10/783,415A   TIME: 09:57:11

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\09142005\J783415A.raw**

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 3 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
 4        REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
 5        HUMAN SERVICES
 6        Marchetti, Antonio
 7        Buttitta, Fiamma
 8        Smith, Gilbert H.
 9        Callahan, Robert
11 <120> TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE
INT6
13 <130> FILE REFERENCE: 4239-67782-01
15 <140> CURRENT APPLICATION NUMBER: 10/783,415A
16 <141> CURRENT FILING DATE: 2004-02-19
18 <150> PRIOR APPLICATION NUMBER: 09/858,152
19 <151> PRIOR FILING DATE: 2001-05-14
21 <150> PRIOR APPLICATION NUMBER: 09/378,842
22 <151> PRIOR FILING DATE: 1999-08-23
24 <150> PRIOR APPLICATION NUMBER: 08/875,847
25 <151> PRIOR FILING DATE: 1997-09-25
27 <150> PRIOR APPLICATION NUMBER: PCT/US96/01884
28 <151> PRIOR FILING DATE: 1996-02-09
30 <150> PRIOR APPLICATION NUMBER: 08/385,998
31 <151> PRIOR FILING DATE: 1995-02-09
33 <160> NUMBER OF SEQ ID NOS: 36
35 <170> SOFTWARE: PatentIn version 3.2
37 <210> SEQ ID NO: 1
38 <211> LENGTH: 1505
39 <212> TYPE: DNA
40 <213> ORGANISM: Murine INT6
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47 ataatgaaaa agaattatta caaggaaaat tagatcttct tagtgatacc aatatggtgg     180
49 actttgctat ggatgtttac aaaaaccttt attctgatga tatccctcat gctttgagag     240
51 aaaaaagaac cacagttgtt gcgcagctga acagctcca ggcagaaaca gaaccaattg      300
53 tgaagatgtt tgaagatcca gaaactacaa ggcagatgca gtcaaccagg gatggcagga     360
55 tgttatttga ctacctggca gacaaacatg ggtttaggca agagtactta gatacactct     420
57 acagatacgc aaaattccag tatgagtgtg gaaattactc tggagctgca gagtatcttt     480
59 acttctttag agttttggtc ccagcaacag atagaaatgc tttaagttcg ctctggggaa     540
61 aactggcctc tgaaatctta atgcagaatt gggatgcagc catggaagac cttactcgat     600
63 taaaagaaac catagacaat aattctgtga gttctccact ccagtctctt cagcagcgaa     660
65 catggctcat tcattggtct ctatttgttt ttttcaacca tccaaagggc cgtgataaca     720
67 ttattgatct cttcctttac caaccacagt atcttaatgc aattcagaca atgtgtccac     780
69 atattctacg ctatttgact actgccgtca taaccaacaa agatgtgcgg aaacgccggc     840
71 aggtgctgaa agatctggtg aaagtgattc aacaggagtc ttacacatat aaagacccaa     900
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73 ttacagaatt tgttgaatgc ctatatgtta actttgattt tgacggggct cagaaaaagc    960
75 tgagagaatg tgaatcagtg ctcgtgaatg acttcttcct ggtagcgtgt ctggaggact   1020
77 tcattgagaa tgcccgtctc ttcatatttg agacgttttg tcgtatccac cagtgtatca   1080
79 gcattaatat gttagcagat aaactgaata tgactccaga agaagctgaa agatggattg   1140
81 tgaatttgat tagaaatgcg aggttggatg ccaagattga ttctaaacta ggtcatgtgg   1200
83 taatgggcaa caatgcagtc tcgccctacc agcaagtgat tgaaaagacc aaaagccttt   1260
85 ctttttagaag ccaaatgttg gccatgaata ttgaaaagaa acttaatcag aacagtagat   1320
87 cagaggctcc caactgggca acccaagact ctggcttcta ttaaaggatt ataaagaaaa   1380
89 gaagaaaaag gaataagtga aagacacagt agccattgtg tataaaggat gacatacatt   1440
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107 Ile Pro His Ala Leu Arg Glu Lys Arg Thr Thr Val Val Ala Gln Leu
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111 Lys Gln Leu Gln Ala Glu Thr Glu Pro Ile Val Lys Met Phe Glu Asp
112         35              40              45
115 Pro Glu Thr Thr Arg Gln Met Gln Ser Thr Arg Asp Gly Arg Met Leu
116     50              55              60
119 Phe Asp Tyr Leu Ala Asp Lys His Gly Phe Arg Gln Glu Tyr Leu Asp
120 65              70              75              80
123 Thr Leu Tyr Arg Tyr Ala Lys Phe Gln Tyr Glu Cys Gly Asn Tyr Ser
124             85              90              95
127 Gly Ala Ala Glu Tyr Leu Tyr Phe Phe Arg Val Leu Val Pro Ala Thr
128             100             105             110
131 Asp Arg Asn Ala Leu Ser Ser Leu Trp Gly Lys Leu Ala Ser Glu Ile
132         115             120             125
135 Leu Met Gln Asn Trp Asp Ala Ala Met Glu Asp Leu Thr Arg Leu Lys
136     130             135             140
139 Glu Thr Ile Asp Asn Asn Ser Val Ser Ser Pro Leu Gln Ser Leu Gln
140 145             150             155             160
143 Gln Arg Thr Trp Leu Ile His Trp Ser Leu Phe Val Phe Asn His
144             165             170             175
147 Pro Lys Gly Arg Asp Asn Ile Ile Asp Leu Phe Leu Tyr Gln Pro Gln
148             180             185             190
151 Tyr Leu Asn Ala Ile Gln Thr Met Cys Pro His Ile Leu Arg Tyr Leu
152         195             200             205
155 Thr Thr Ala Val Ile Thr Asn Lys Asp Val Arg Lys Arg Arg Gln Val
156     210             215             220
159 Leu Lys Asp Leu Val Lys Val Ile Gln Gln Glu Ser Tyr Thr Tyr Lys
160 225             230             235             240
163 Asp Pro Ile Thr Glu Phe Val Glu Cys Leu Tyr Val Asn Phe Asp Phe
164             245             250             255
167 Asp Gly Ala Gln Lys Lys Leu Arg Glu Cys Glu Ser Val Leu Val Asn
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171 Asp Phe Phe Leu Val Ala Cys Leu Glu Asp Phe Ile Glu Asn Ala Arg
172          275               280               285
175 Leu Phe Ile Phe Glu Thr Phe Cys Arg Ile His Gln Cys Ile Ser Ile
176      290               295               300
179 Asn Met Leu Ala Asp Lys Leu Asn Met Thr Pro Glu Glu Ala Glu Arg
180 305              310               315               320
183 Trp Ile Val Asn Leu Ile Arg Asn Ala Arg Leu Asp Ala Lys Ile Asp
184              325               330               335
187 Ser Lys Leu Gly His Val Val Met Gly Asn Asn Ala Val Ser Pro Tyr
188          340               345               350
191 Gln Gln Val Ile Glu Lys Thr Lys Ser Leu Ser Phe Arg Ser Gln Met
192      355               360               365
195 Leu Ala Met Asn Ile Glu Lys Lys Leu Asn Gln Asn Ser Arg Ser Glu
196      370               375               380
199 Ala Pro Asn Trp Ala Thr Gln Asp Ser Gly Phe Tyr
200 385              390               395
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204 <211> LENGTH: 1500
205 <212> TYPE: DNA
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 3
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213 aaaaggaatt attacaaggt aaattggacc ttcttagtga taccaacatg gtagactttg   180
215 ctatggatgt atacaaaaac cttttattct atgatattcc tcatgctttg agagagaaaa   240
217 gaaccacagt ggttgcacaa ctgaaacagc ttcaggcaga aacagaacca attgtgaaga   300
219 tgtttgaaga tccagaaact acaaggcaaa tgcagtcaac cagggatggt aggatgctct   360
221 ttgactacct ggcggacaag catggtttta ggcaggaata tttagataca ctctacagat   420
223 atgcaaaatt ccagtacgaa tgtgggaatt actcaggagc agcagaatat ctttattttt   480
225 ttagagtgct ggttccagca acagatagaa atgctttaag ttcactctgg ggaaagctgg   540
227 cctctgaaat cttaatgcag aattgggatg cagccatgga agaccttaca cggttaaaag   600
229 agaccataga taataattct gtgagttctc cacttcagtc tcttcagcag agaacatggc   660
231 tcattcactg gtctctgttt gttttcttca atcaccccaa aggtcgcgat aatattattg   720
233 acctcttcct ttatcagcca caatatctta atgcaattca gacaatgtgt ccacacattc   780
235 ttcgctattt gactacagca gtcataacaa acaaggatgt tcgaaacgt cggcaggttc   840
237 taaaagatct agttaaagtt attcaacagg agtcttacac atataaagac ccaattacag   900
239 aatttgttga atgtttatat gttaactttg actttgatgg ggctcagaaa aagctgaggg   960
241 aatgtgaatc agtgcttgtg aatgacttct tcttggtggc ttgtcttgag gatttcattg  1020
243 aaaatgcccg tctcttcata tttgagactt tctgtcgcat ccaccagtgt atcagcatta  1080
245 acatgttggc agataaattg aacatgactc cagaagaagc tgaaaggtgg attgtaaatt  1140
247 tgattagaaa tgcaagactg gatgccaaga ttgattctaa attaggtcat gtggttatgg  1200
249 gtaacaatgc agtctcaccc tatcagcaag tgattgaaaa gaccaaaagc ctttcctta   1260
251 gaagccagat gttggccatg aatattgaga agaaacttaa tcagaatagc aggtcagagg  1320
253 ctcctaactg ggcaactcaa gattctggct ctactgaag aaccataaag aaaagatgaa  1380
255 aaaaaaaact atcaaagaaa gatgaaataa taaaactatt atataaaggg tgacttacat  1440
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261 <211> LENGTH: 396
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262 <212> TYPE: PRT
263 <213> ORGANISM: Homo sapiens
265 <400> SEQUENCE: 4
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268 1               5                   10                  15
271 Ile Pro His Ala Leu Arg Glu Lys Arg Thr Thr Val Val Ala Gln Leu
272             20                  25                  30
275 Lys Gln Leu Gln Ala Glu Thr Glu Pro Ile Val Lys Met Phe Glu Asp
276         35                  40                  45
279 Pro Glu Thr Thr Arg Gln Met Gln Ser Thr Arg Asp Gly Arg Met Leu
280     50                  55                  60
283 Phe Asp Tyr Leu Ala Asp Lys His Gly Phe Arg Gln Glu Tyr Leu Asp
284 65                  70                  75                  80
287 Thr Leu Tyr Arg Tyr Ala Lys Phe Gln Tyr Glu Cys Gly Asn Tyr Ser
288             85                  90                  95
291 Gly Ala Ala Glu Tyr Leu Tyr Phe Phe Arg Val Leu Val Pro Ala Thr
292             100                 105                 110
295 Asp Arg Asn Ala Leu Ser Ser Leu Trp Gly Lys Leu Ala Ser Glu Ile
296         115                 120                 125
299 Leu Met Gln Asn Trp Asp Ala Ala Met Glu Asp Leu Thr Arg Leu Lys
300     130                 135                 140
303 Glu Thr Ile Asp Asn Asn Ser Val Ser Ser Pro Leu Gln Ser Leu Gln
304 145                 150                 155                 160
307 Gln Arg Thr Trp Leu Ile His Trp Ser Leu Phe Val Phe Phe Asn His
308             165                 170                 175
311 Pro Lys Gly Arg Asp Asn Ile Ile Asp Leu Phe Leu Tyr Gln Pro Gln
312             180                 185                 190
315 Tyr Leu Asn Ala Ile Gln Thr Met Cys Pro His Ile Leu Arg Tyr Leu
316         195                 200                 205
319 Thr Thr Ala Val Ile Thr Asn Lys Asp Val Arg Lys Arg Arg Gln Val
320     210                 215                 220
323 Leu Lys Asp Leu Val Lys Val Ile Gln Gln Glu Ser Tyr Thr Tyr Lys
324 225                 230                 235                 240
327 Asp Pro Ile Thr Glu Phe Val Glu Cys Leu Tyr Val Asn Phe Asp Phe
328             245                 250                 255
331 Asp Gly Ala Gln Lys Lys Leu Arg Glu Cys Glu Ser Val Leu Val Asn
332             260                 265                 270
335 Asp Phe Phe Leu Val Ala Cys Leu Glu Asp Phe Ile Glu Asn Ala Arg
336         275                 280                 285
339 Leu Phe Ile Phe Glu Thr Phe Cys Arg Ile His Gln Cys Ile Ser Ile
340     290                 295                 300
343 Asn Met Leu Ala Asp Lys Leu Asn Met Thr Pro Glu Glu Ala Glu Arg
344 305                 310                 315                 320
347 Trp Ile Val Asn Leu Ile Arg Asn Ala Arg Leu Asp Ala Lys Ile Asp
348             325                 330                 335
351 Ser Lys Leu Gly His Val Val Met Gly Asn Asn Ala Val Ser Pro Tyr
352             340                 345                 350
355 Gln Gln Val Ile Glu Lys Thr Lys Ser Leu Ser Phe Arg Ser Gln Met
356             355                 360                 365
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359 Leu Ala Met Asn Ile Glu Lys Lys Leu Asn Gln Asn Ser Arg Ser Glu
360     370             375             380
363 Ala Pro Asn Trp Ala Thr Gln Asp Ser Gly Phe Tyr
364 385             390             395
367 <210> SEQ ID NO: 5
368 <211> LENGTH: 25
369 <212> TYPE: DNA
370 <213> ORGANISM: Artificial Sequence
372 <220> FEATURE:
373 <223> OTHER INFORMATION: Oligonucleotide primer
375 <400> SEQUENCE: 5
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380 <211> LENGTH: 20
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382 <213> ORGANISM: Artificial Sequence
384 <220> FEATURE:
385 <223> OTHER INFORMATION: Oligonucleotide primer
387 <400> SEQUENCE: 6
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392 <211> LENGTH: 20
393 <212> TYPE: DNA
394 <213> ORGANISM: Artificial Sequence
396 <220> FEATURE:
397 <223> OTHER INFORMATION: Oligonucleotide primer
399 <400> SEQUENCE: 7
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404 <211> LENGTH: 22
405 <212> TYPE: DNA
406 <213> ORGANISM: Artificial Sequence
408 <220> FEATURE:
409 <223> OTHER INFORMATION: Oligonucleotide primer
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416 <211> LENGTH: 20
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418 <213> ORGANISM: Artificial Sequence
420 <220> FEATURE:
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428 <211> LENGTH: 20
429 <212> TYPE: DNA
430 <213> ORGANISM: Artificial Sequence
432 <220> FEATURE:
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VERIFICATION SUMMARY   DATE: 09/14/2005
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